

Appendix I: Alignment of the CMV IE enhancer of M60321 with instant SEQ ID NO: 3

BLASTN 2.2.25+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: N05YT4ZW111

Query= gi|330624|gb|M60321.1|HS5MIEP Human cytomegalovirus major immediate-early protein gene, 5' end

Length=2361

		Score (Bits)	E Value
Sequences producing significant alignments:			
lcl 26147	SID_3	977	0.0

ALIGNMENTS

>lcl|26147 SID_3

Length=3584

Score = 977 bits (529), Expect = 0.0
 Identities = 543/549 (99%), Gaps = 3/549 (0%)
 Strand=Plus/Plus

Query 535	ACCGCCATGTTGACATTGATTGACTAGTTATTAAATAGTAATCAATTACGGGGTCATT	594
Sbjct 29	ACCGCCATGTTGACATTGATTGACTAGTTATTAAATAGTAATCAATTACGGGGTCATT	88
Query 595	AGTCATAGCCCCATATATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCCTCG	654
Sbjct 89	AGTCATAGCCCCATATATGGAGTTCCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGG	148
Query 655	-TGACCGCCCAACGACCCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAAC	713
Sbjct 149	CTGACCGCCCAACGACCCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAC	208
Query 714	GCCAATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTT	773
Sbjct 209	GCCAATAGGGACTTCCATTGACGTCAATGGGTGGAGTATTACGGTAAACTGCCACTT	268
Query 774	GGCAGTACATCAAGTGTATCATATGCCAAGTCCGGCCCCCTATTGACGTCAATGACGGTA	833
Sbjct 269	GGCAGTACATCAAGTGTATCATATGCCAAGTCC-GCCCCCTATTGACGTCAATGACGGTA	327
Query 834	AATGGCCCGCCTGGCATTATGCCAGTACATGACCTTACGGACTTCTACTTGGCAGT	893
Sbjct 328	AATGGCCCGCCTGGCATTATGCCAGTACATGACCTTACGGACTTCTACTTGGCAGT	387
Query 894	ACATCTACGTATTAGTCATCGCTATTACCATGGT-GATGCGTTTGGCAGTACACCAAT	952
Sbjct 388	ACATCTACGTATTAGTCATCGCTATTACCATGGTGGATGCGTTTGGCAGTACACCAAT	447
Query 953	GGGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT	1012
Sbjct 448	GGGCGTGGATAGCGGTTGACTCACGGGATTCCAAGTCTCCACCCATTGACGTCAAT	507

Query	1013	GGGAGTTGTTGGCACAAAATCAACGGGACTTCCAAAATGTCGTAATAACCCGCC	1072
Sbjct	508	GGGAGTTGTTGGCACAAAATCAACGGGACTTCCAAAATGTCGTAATAACCCGCC	567
Query	1073	CCGTTGACG 1081	
Sbjct	568	CCGTTGACG 576	